



41426-FA-PCT-US
SEQUENCE LISTING

<110> Israeli, Ron S.

Heston, Warren D.W.

Fair, William R.

<120> PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND USES THEREOF

<130> 1769/41426-FA-PCT-US

<140> 10/751,346

<141> 1998-01-02

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taaataaatt atttccaagt gttgaaggaa attcagactt ctaatttgct ctgattctga	480
aactaaaaca aatgctctgt gagagtttgc gtttccagtg aagtagcgtg agaaatccaa	540
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aagagtccat ttctattagg taagttcctt tagtcctttt attactgggc actcttaatt     1140
acatgtagct tgaaatatgt ccagtttgag cagtgaactg aaaatgtcat gtgattaagt     1200
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ccagcactat gctagaagtt gtgaagaatt cacgagatga ataaatcaca gattctgtcc      180
tcaaaatggt tagatctatt caggaaacaa agctaaaaaa accccaccaa taactaaaaa      240
tcaaccaaat gaaaaacaac aatcataaaa taagtaagta cctatagaaa gaaaagctca      300
gaggaggtaa aaagataact cttccaaaag gaatactata tactgtaaac tgtgtactga      360
tagaaggaag aattagaaan nnnnnnntgt aagtggcata cataactaagc tagtgtgaac      420
acaagcctaa atatgtagtt gcttcacaga aggttagaag taaattaacc tcatgaattt      480
cttgagagaa cttgtaagga ctaagcttcc gattttggag aaagatttta ataccataa      540
aaaagtacct ttgtttggta atctcaatca ttataatagt gcttagataa tacctaggaa      600
caaattaaat attaaattta ctttaaaaaa aagtacatga ttggggaatc acaactggcc      660
ttactagatt ctctnnnnnn atatgcactg aaaagaatga aaaacactga accaaatatn      720
tgttttttta agttttaaata taaattggaa aaaaatagta aggaatatca gaagcaaaaa      780
aataaaatga aagcaagaat cctcagaggt agcacgaaat ttggctttgc ttagatggat      840
ctatcaaagc tatggcccat gaaaaggatt caggagttag tttaaagctg gttcacataa      900
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tgagggggct cacnctnaat nccagcactt tgggagccca aggtgggtgg atcacgaggt     1020
caggagtttg agaccagcct gaccaacatg gtgaaaccgc gtctctacta aaaatagaaa     1080
aattagccgn gcctacgtgc ttctaattcc agctgaactc aggagactga gacaggagaa     1140
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<211> 783

<212> DNA

<213> HOMO SAPIENS

<400> 124

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atgccacct tacagagagg acacatttac taggttatat cccgggggta aattcgagca      180
ttggaatttg gccagtgtag atgttttagag tgaacagaac aaatttttct gtgcttacag      240
gttatggctg tggcctacaa gaagcatgca ctgggtttat tattaacttt cagtatcttt      300
gttttaaata ttttctacaa aaatgtttac taaattaaat tgtagtatga attgttataa      360
ataatgaggg aaaacaattt acacatagca aatttaaaaa ttactgtcat ttgatttggt      420
aatatatttt tctcttttagt gggaaattaa attttaaaaa attccctttc gactgtagaa      480
caaataggaa tttggcctgt ggggtctact tgcttattat atttgtaagc tagtggtagg      540
aaatagcaaa tgctcactac cactaataag aacatttcta aatctgatgt tctgaggatt      600
tttagagctt atagtagcaa aaagaaaagg gaaattctat ccgagatgtc ctttggtgta      660
ggcctaataa gaaaagggtg aagataaagt tctggtactc atttaagtgt aatattgaaa      720
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tct                                                                    783

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cctacaacaa aggacatctc ggatagaatt tcccttttct ttttgctact ataagctcta      180

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aaaatcctca gaacatcaga tttagaaatg ttcttattag tggtagtgag catttgctat	240
ttcctaccac tagcttacia atataataag caagtagacc ccacaggcca aattcctatt	300
tgttctacag tcgaaagga attttttaaa atttaatttc ccactaaaga gaaaaatata	360
ttaacaaatc aaatgacagt aatttttaaa tttgctatgt gtaaattggt ttccctcatt	420
atttataaca attcatacta caatttaatt tagtaaacad ttttgtagaa aatatttaaa	480
acaaagatac tgaaagttaa tatnaaaccc agtgcattgt tcttgtaggc cacagccata	540
acctgtaagc acagaaaaat ttgttctgtt actctaaaca tctacactgg ccaaattcca	600
atgctcgaat ttaaccccggt gatataacct agtaaattgt tcctctctgt aagggtgggca	660
tgacacagaa tacaagaaaa taatggtatt cataaagttt taagaaaatg attctacaca	720
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<222> (917)..(917)

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<222> (1009)..(1009)

<223> n=any nucleotide

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ttgctttgaa	cccactatat	tnnnnnnnct	cgggcaatga	ctcagtgtgg	caaggatact		300	
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ccttgatagc	tcttaaatag	atgctgcacc	aacactctct	ttcttttctc	tctttttctt		420	
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nnnnnnnttt	caccatngct	gatcaggctg	gtctcgaact	cctgaccgca	gtgantccgc		960	
cctccttggc	ctcccaaagt	gctgagatta	caggcatgag	tactg	cgnc	cagccaccat	1020	

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<210> 127

<211> 1977

<212> DNA

<213> HOMO SAPIENS

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gcacaggagg	cttagataac	atgccc aaag	tc atgcttct	agtaa atgga	tataattaag		240
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cgctttccag	agcatgtgct	gttgatagag	cttgatgtct	aactctctga	aattttccat		360
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aaaggcaaaa	aatgagccgg	gcatggtggc	acatgccttg	cacatcccag	ctgaggcagg		1860
agaattcact	tgaacctggg	aggtagagat	tgcggtgaag	cgagatcacg	tcattgcact		1920

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1977

<210> 128

<211> 750

<212> PRT

<213> Homo sapiens

<400> 128

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Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly Gly Phe
20 25 30

Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser Ser Asn Glu
35 40 45

Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala Phe Leu Asp Glu
50 55 60

Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr Asn Phe Thr Gln Ile
65 70 75 80

Pro His Leu Ala Gly Thr Glu Gln Asn Phe Gln Leu Ala Lys Gln Ile
85 90 95

Gln Ser Gln Trp Lys Glu Phe Gly Leu Asp Ser Val Glu Leu Ala His
100 105 110

Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn Tyr Ile
115 120 125

Ser Ile Ile Asn Glu Asp Gly Asn Glu Ile Phe Asn Thr Ser Leu Phe
130 135 140

Glu Pro Pro Pro Pro Gly Tyr Glu Asn Val Ser Asp Ile Val Pro Pro
145 150 155 160

Phe Ser Ala Phe Ser Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr
165 170 175

Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met
180 185 190

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Lys Ile Asn Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val
 195 200 205

Phe Arg Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly
 210 215 220

Val Ile Leu Tyr Ser Asp Pro Ala Asp Tyr Phe Ala Pro Gly Val Lys
 225 230 235 240

Ser Tyr Pro Asp Gly Trp Asn Leu Pro Gly Gly Gly Val Gln Arg Gly
 245 250 255

Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro Gly Tyr
 260 265 270

Pro Ala Asn Glu Tyr Ala Tyr Arg Arg Gly Ile Ala Glu Ala Val Gly
 275 280 285

Leu Pro Ser Ile Pro Val His Pro Ile Gly Tyr Tyr Asp Ala Gln Lys
 290 295 300

Leu Leu Glu Lys Met Gly Gly Ser Ala Pro Pro Asp Ser Ser Trp Arg
 305 310 315 320

Gly Ser Leu Lys Val Pro Tyr Asn Val Gly Pro Gly Phe Thr Gly Asn
 325 330 335

Phe Ser Thr Gln Lys Val Lys Met His Ile His Ser Thr Asn Glu Val
 340 345 350

Thr Arg Ile Tyr Asn Val Ile Gly Thr Leu Arg Gly Ala Val Glu Pro
 355 360 365

Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser Trp Val Phe Gly
 370 375 380

Gly Ile Asp Pro Gln Ser Gly Ala Ala Val Val His Glu Ile Val Arg
 385 390 395 400

Ser Phe Gly Thr Leu Lys Lys Glu Gly Trp Arg Pro Arg Arg Thr Ile
 405 410 415

Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Leu Leu Gly Ser Thr
 420 425 430

Glu Trp Ala Glu Glu Asn Ser Arg Leu Leu Gln Glu Arg Gly Val Ala
 435 440 445

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Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly Asn Tyr Thr Leu Arg Val
 450 455 460

Asp Cys Thr Pro Leu Met Tyr Ser Leu Val His Asn Leu Thr Lys Glu
 465 470 475 480

Leu Lys Ser Pro Asp Glu Gly Phe Glu Gly Lys Ser Leu Tyr Glu Ser
 485 490 495

Trp Thr Lys Lys Ser Pro Ser Pro Glu Phe Ser Gly Met Pro Arg Ile
 500 505 510

Ser Lys Leu Gly Ser Gly Asn Asp Phe Glu Val Phe Phe Gln Arg Leu
 515 520 525

Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr Lys Asn Trp Glu Thr Asn
 530 535 540

Lys Phe Ser Gly Tyr Pro Leu Tyr His Ser Val Tyr Glu Thr Tyr Glu
 545 550 555 560

Leu Val Glu Lys Phe Tyr Asp Pro Met Phe Lys Tyr His Leu Thr Val
 565 570 575

Ala Gln Val Arg Gly Gly Met Val Phe Glu Leu Ala Asn Ser Ile Val
 580 585 590

Leu Pro Phe Asp Cys Arg Asp Tyr Ala Val Val Leu Arg Lys Tyr Ala
 595 600 605

Asp Lys Ile Tyr Ser Ile Ser Met Lys His Pro Gln Glu Met Lys Thr
 610 615 620

Tyr Ser Val Ser Phe Asp Ser Leu Phe Ser Ala Val Lys Asn Phe Thr
 625 630 635 640

Glu Ile Ala Ser Lys Phe Ser Glu Arg Leu Gln Asp Phe Asp Lys Ser
 645 650 655

Asn Pro Ile Val Leu Arg Met Met Asn Asp Gln Leu Met Phe Leu Glu
 660 665 670

Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg
 675 680 685

His Val Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser
 690 695 700

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Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp
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Pro Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Tyr Val Ala Ala
 725 730 735

Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala
 740 745 750